AMENDMENT

In the Claims:

Please amend the claims as follows:

Please cancel claims 1-12, without prejudice or disclaimer.

Please add new claims 13-31 as follows:

1-12. (Canceled)

13. (New) A method for analyzing DNA of a sweet potato comprising:

providing sweet potato DNA;

breaking the DNA into pieces;

introducing a known sequence at at least one end of the DNA pieces;

providing at least a first primer of formula:

$(N_x)_nAGTCCTAACAN_1N_2N_3$ (I)

wherein N_x is selected from A, C, G and T; n is 0 to 20; N_1 is G, T, A or not present; N_2 is A, C, G or not present; and N_3 is A, C, G or not present; or a complementary sequence thereto; and at least a second primer capable of annealing to the introduced sequence;

amplifying DNA of the DNA pieces with the primers; and

analyzing the amplified DNA.

14. (New) The method of claim 13, wherein breaking the DNA into pieces involves digestion by a restriction endonuclease.

15. (New) The method of claim 14, wherein the restriction endonuclease is a 6 base pair cutting restriction endonuclease.

16. (New) The method of claim 15, wherein the restriction endonuclease is a rare cutting enzyme.

17. (New) The method of claim 13, wherein $(N_x)_4$ residue comprises the sequence AGACTAAG.

18. (New) The method of claim 13, wherein the first primer has a sequence of: AGACTAAGAGTCCTAACA (SEQ ID NO:3), AGACTAAGAGTCCTAACAG (SEQ ID NO:4), AGACTAAGAGTCCTAACAT (SEQ ID NO:5), AGACTAAGAGTCCTAACAA (SEQ ID NO:6), AGACTAAGAGTCCTAACAGC (SEQ ID NO:7), AGACTAAGAGTCCTAACAGA (SEQ ID NO:8), AGACTAAGAGTCCTAACAGG (SEQ ID NO:9), AGACTAAGAGTCCTAACATA (SEQ ID NO:10), AGACTAAGAGTCCTAACATG (SEQ ID NO:11), AGACTAAGAGTCCTAACATC (SEQ ID NO:12), AGACTAAGAGTCCTAACAAA (SEQ ID NO:13), AGACTAAGAGTCCTAACAAG (SEQ ID NO:14), AGACTAAGAGTCCTAACAAC (SEQ ID NO:15), or a fragment thereof.

19. (New) The method of claim 13, wherein the first primer is a fragment of a sequence of AGACTAAGAGTCCTAACA (SEQ ID NO:3), AGACTAAGAGTCCTAACAG (SEQ ID NO:4), AGACTAAGAGTCCTAACAT (SEQ ID NO:5), AGACTAAGAGTCCTAACAA (SEQ ID NO:6), AGACTAAGAGTCCTAACAGC (SEQ ID NO:7), AGACTAAGAGTCCTAACAGA (SEQ ID NO:8), AGACTAAGAGTCCTAACAGG (SEQ ID NO:9), AGACTAAGAGTCCTAACATA (SEQ ID NO:10), AGACTAAGAGTCCTAACATG (SEQ ID NO:11), AGACTAAGAGTCCTAACATC (SEQ ID NO:12), AGACTAAGAGTCCTAACAAA (SEQ ID NO:13), AGACTAAGAGTCCTAACAAG (SEQ ID NO:14), AGACTAAGAGTCCTAACAAC (SEQ ID NO:15) and is further defined as comprising at least 10 base pairs of a 3' region of the sequence.

20. (New) The method of claim 13, wherein introducing known sequences at at least one of end of the DNA pieces comprises cutting the DNA with a restriction enzyme and linking an adapter to the end, the adapter comprising a known sequence.

21. (New) The method of claim 13, wherein analyzing the amplified DNA comprises separating the amplified nucleic acid molecules by size.

22. (New) The method of claim 13, further defined as a method of defining phylogenetic and/or geographical relationships of two or more sweet potatoes having different genotypes.

23. (New) The method of claim 22, comprising analyzing the DNA of a first sweet potato and analyzing the DNA of a second sweet potato and comparing the results.

24. (New) The method of claim 23, wherein comparing the results is further defined as comparing a size separation of amplified nucleic acids from the first sweet potato with a size separation of amplified nucleic acids from the second sweet potato.

25. (New) The method of claim 23, wherein comparing the results comprises using a computer to calculate the phylogenetic distance from a size separation of amplified nucleic acids.

26. (New) A kit comprising a first primer of formula:

$(N_x)_nAGTCCTAACAN_1N_2N_3$ (I)

wherein N_x is selected from A, C, G and T; n is 0 to 20; N_1 is G, T, A or not present; N_2 is A, C, G or not present; and N_3 is A, C, G or not present; or a complementary sequence thereto;

at least a second primer; and

a nucleic acid polymerase.

27. (New) The kit of claim 26, wherein $(N_x)_4$ residue comprises the sequence AGACTAAG.

28. (New) The kit of claim 26, wherein the first primer has a sequence of: AGACTAAGAGTCCTAACA (SEQ ID NO:3), AGACTAAGAGTCCTAACAG (SEQ ID NO:4), AGACTAAGAGTCCTAACAT (SEQ ID NO:5), AGACTAAGAGTCCTAACAA (SEQ ID NO:6), AGACTAAGAGTCCTAACAGC (SEQ ID NO:7), AGACTAAGAGTCCTAACAGA (SEQ ID NO:8), AGACTAAGAGTCCTAACAGG (SEQ ID NO:9), AGACTAAGAGTCCTAACATA (SEQ ID NO:10), AGACTAAGAGTCCTAACATG (SEQ ID NO:11), AGACTAAGAGTCCTAACATC (SEQ ID NO:12), AGACTAAGAGTCCTAACAAA (SEQ ID NO:13), AGACTAAGAGTCCTAACAAG (SEQ ID NO:14), AGACTAAGAGTCCTAACAAC (SEQ ID NO:15), or a fragment thereof.

29. (New) The kit of claim 26, wherein the first primer is a fragment of a sequence of AGACTAAGAGTCCTAACA (SEQ ID NO:3), AGACTAAGAGTCCTAACAG (SEQ ID NO:4), AGACTAAGAGTCCTAACAT (SEQ ID NO:5), AGACTAAGAGTCCTAACAA (SEQ ID NO:6), AGACTAAGAGTCCTAACAGC (SEQ ID NO:7), AGACTAAGAGTCCTAACAGA (SEQ ID NO:8), AGACTAAGAGTCCTAACAGG (SEQ

ID NO:9), AGACTAAGAGTCCTAACATA (SEQ ID NO:10), AGACTAAGAGTCCTAACATG (SEQ ID NO:11), AGACTAAGAGTCCTAACATC (SEQ ID NO:12), AGACTAAGAGTCCTAACAAA (SEQ ID NO:13), AGACTAAGAGTCCTAACAAG (SEQ ID NO:14), AGACTAAGAGTCCTAACAAC (SEQ ID NO:15) and is further defined as comprising at least 10 base pairs of a 3' region of the sequence.

30. (New) A nucleic acid molecule comprising a sequence of from between 12 and 286 base pairs of SEQ ID NO:1, a sequence differing by not more than 1 base per 20 base pairs from the sequence of SEQ ID NO:1, a sequence that hybridizes under stringent conditions to the sequence of SEQ ID NO:1, or a sequence that is complementary to any of these.

31. (New) The nucleic acid molecule of claim 13, further defined as comprising SEQ ID NO:1.